

(A)

Tue Jul 17 13:47:10 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpenda/templ/ss.DNA32292 (1364 bp)

Sequences producing High-scoring Segment Pairs:					Frame	Score	Match	Pct	E-val
1	P_AAC97409	Human angiogenesis-associated protein PR			+	1364	1364	100	0.0
2	P_AAF72371	Human PRO211 cDNA.			+	1364	1364	100	0.0
3	P_AAF60360	PRO211 coding sequence.			+	1364	1364	100	0.0
4	P_AAZ93700	PRO211 DNA32292-1131.			+	1364	1364	100	0.0
5	P_AAA30040	Human PRO211 nucleotide sequence.			+	1364	1364	100	0.0
6	P_AAA54089	PRO211 cDNA.			+	1364	1364	100	0.0
7	P_AAX28433	EGF-like homologue PRO211 coding sequenc			+	1364	1364	100	0.0
8	P_AAX52213	Protein PRO211 cDNA clone DNA32292-1131.			+	1364	1364	100	0.0
9	P_AAX37671	Human EGF-like homologue (PRO217) encode			+	1364	1364	100	0.0
10	AX076909	Sequence 21 from Patent WO0105836.			+	1364	1364	100	0.0
11	P_AAF29457	Human TANGO 331 cDNA.			+	1350	1350	100	0.0
12	P_AAA08503	DNA encoding human apoptosis related pro			+	1290	1358	99	0.0
13	P_AAC76920	Human ORFX ORF2475 polynucleotide sequen			+	1208	1215	100	0.0

>1 P_AAC97409 Human angiogenesis-associated protein PRO211 cDNA, SEQ ID NO:56.
(1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

DNA32292	1	GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

P_AAC97409	1	GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

P_AAC97409	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

P_AAC97409	121	GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGGAACACGGC

P_AAC97409	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT

P_AAC97409	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

P_AAC97409	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

P_AAC97409	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC

P_AAC97409	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGGAGATGGGAG

BLAST ~~REPORT~~ RESULTS A-1

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*****
P_AAC97409 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292 541 CAGACAGGGCGACGGGTCCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
*****
P_AAC97409 541 CAGACAGGGCGACGGGTCCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
DNA32292 601 CTGCATGGACGGCTACTTCAGCTCGTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
*****
P_AAC97409 601 CTGCATGGACGGCTACTTCAGCTCGTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
*****
P_AAC97409 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
*****
P_AAC97409 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
*****
P_AAC97409 781 TCCCTGCAGCGCTGCGCAGTTCTGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTC
*****
P_AAC97409 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTC
DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
*****
P_AAC97409 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****
P_AAC97409 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
*****
P_AAC97409 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
*****
P_AAC97409 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292 1141 CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
*****
P_AAC97409 1141 CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC
*****
P_AAC97409 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC
DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
P_AAC97409 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****

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BLAST RESULTS A-2

P_AAC97409 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>2 P_AAF72371 Human PRO211 cDNA. (1825 bp) [1 seg]

Score = 1364 (2704 bits), Expect. = 0.0

Identities = 1364/1364 (100%), at 1,75-1364,1438, Strand +/-

DNA32292	1	GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

P_AAF72371	75	GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

P_AAF72371	135	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

P_AAF72371	195	GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

P_AAF72371	255	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCTGCTGGAGATCCT

P_AAF72371	315	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

P_AAF72371	375	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

P_AAF72371	435	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGAACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC

P_AAF72371	495	TTGTGTGAAGAACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG

P_AAF72371	555	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA

P_AAF72371	615	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

P_AAF72371	675	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

P_AAF72371	735	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

P_AAF72371	795	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

BLAST RESULTS #3

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DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
*****
P_AAF72371 855 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

DNA32292 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGATCTC
*****
P_AAF72371 915 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGATCTC

DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA
*****
P_AAF72371 975 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA

DNA32292 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****
P_AAF72371 1035 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
*****
P_AAF72371 1095 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

DNA32292 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
*****
P_AAF72371 1155 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

DNA32292 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT
*****
P_AAF72371 1215 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT

DNA32292 1201 GCAGTGGACAGCGGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
*****
P_AAF72371 1275 GCAGTGGACAGCGGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
P_AAF72371 1335 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
P_AAF72371 1395 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

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BLAST RESULTS A-4

>3 P_AAF60360 PRO211 coding sequence. (1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/+

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DNA32292 1 GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAF60360 1 GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAF60360 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
P_AAF60360 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

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DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACCTTTGGCGGCGGGAACACGGC
P_AAF60360	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACCTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATCCT
P_AAF60360	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
P_AAF60360	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
P_AAF60360	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
P_AAF60360	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
P_AAF60360	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
P_AAF60360	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
P_AAF60360	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
P_AAF60360	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
P_AAF60360	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
P_AAF60360	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
P_AAF60360	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
P_AAF60360	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
P_AAF60360	961	AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGCGCAGAGGCTGAAGCCAC

BLAST RESULTS A-5

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*****
P_AAF60360 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292 1081 AGAAGGAGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
*****
P_AAF60360 1081 AGAAGGAGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
*****
P_AAF60360 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
*****
P_AAF60360 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
P_AAF60360 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
P_AAF60360 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

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>4 P_AAZ93700 PRO211 DNA32292-1131. (1364 bp) [1 seg]
 Score = 1364 (2704 bits), Expect = 0.0
 Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

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DNA32292 1 GGCCGGAGCAGCACGGCCGCGAGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAZ93700 1 GGCCGGAGCAGCACGGCCGCGAGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAZ93700 61 CGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
P_AAZ93700 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
*****
P_AAZ93700 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCCTGCTGGAGATCCT
*****
P_AAZ93700 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCCTGCTGGAGATCCT
DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCCAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAZ93700 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCCAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAZ93700 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****

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BLAST RESULTS A-U

P_AA93700	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG *****
P_AA93700	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCTGCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA *****
P_AA93700	541	CAGACAGGGCGACGGGTCTGCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG *****
P_AA93700	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT *****
P_AA93700	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC *****
P_AA93700	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG *****
P_AA93700	781	TCCCTGCAGCGCTGCGCAGTTCTGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC *****
P_AA93700	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA *****
P_AA93700	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG *****
P_AA93700	961	AACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC *****
P_AA93700	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC *****
P_AA93700	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292	1141	CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT *****
P_AA93700	1141	CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC *****
P_AA93700	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC
DNA32292	1261	TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT *****
P_AA93700	1261	TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

BLAST RESULTS A-7

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DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAAA
*****
P_AA293700 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAAA

>5 P_AAA30040 Human PRO211 nucleotide sequence. (1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

DNA32292      1 GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAA30040      1 GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292     61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAA30040     61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292    121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
P_AAA30040    121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

DNA32292    181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
*****
P_AAA30040    181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

DNA32292    241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
*****
P_AAA30040    241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

DNA32292    301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAA30040    301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

DNA32292    361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAA30040    361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

DNA32292    421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****
P_AAA30040    421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC

DNA32292    481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
*****
P_AAA30040    481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG

DNA32292    541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
*****
P_AAA30040    541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA

DNA32292    601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
*****
P_AAA30040    601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

DNA32292    661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
*****
P_AAA30040    661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

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BLAST RESULTS A-B


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DNA32292 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
*****
P_AAA30040 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
*****
P_AAA30040 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

DNA32292 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGATCTC
*****
P_AAA30040 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGATCTC

DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA
*****
P_AAA30040 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA

DNA32292 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****
P_AAA30040 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
*****
P_AAA30040 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

DNA32292 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
*****
P_AAA30040 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

DNA32292 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
*****
P_AAA30040 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT

DNA32292 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
*****
P_AAA30040 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

DNA32292 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGATATTTTGATACAGTTCTT
*****
P_AAA30040 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGATATTTTGATACAGTTCTT

DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
P_AAA30040 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

```

>6 P_AAA54089 PRO211 cDNA. (1364 bp) [1 seg]

Score = 1364 (2704 bits), Expect = 0.0

Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

```

DNA32292 1 GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAA54089 1 GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAA54089 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

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BLAST RESULTS A-9

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*****
P_AAA54089 121 GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
*****
P_AAA54089 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCCTGCTGGAGATCCT
*****
P_AAA54089 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCCTGCTGGAGATCCT
DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAA54089 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAA54089 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****
P_AAA54089 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
*****
P_AAA54089 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
*****
P_AAA54089 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
DNA32292 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
*****
P_AAA54089 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
*****
P_AAA54089 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
*****
P_AAA54089 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
*****
P_AAA54089 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAACTGTAAAGAGTGTATCTC
*****
P_AAA54089 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAACTGTAAAGAGTGTATCTC
DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
*****
P_AAA54089 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****

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BLAST RESULTS A-10

P_AAA54089 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

P_AAA54089 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

DNA32292 1081 AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

P_AAA54089 1081 AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

DNA32292 1141 CCTTTAAATTATTCAGAAGGATGTCCCGTGAAAAATGTGGCCCTGAGGATGCCGTCTCCT

P_AAA54089 1141 CCTTTAAATTATTCAGAAGGATGTCCCGTGAAAAATGTGGCCCTGAGGATGCCGTCTCCT

DNA32292 1201 GCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTAACGGTTGATTCTCATTTGTCCC

P_AAA54089 1201 GCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTAACGGTTGATTCTCATTTGTCCC

DNA32292 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

P_AAA54089 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

P_AAA54089 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>7 P_AAX28433 EGF-like homologue PRO211 coding sequence. DNA, PAT 22-JUN-1999
(1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/-

DNA32292 1 GGCCGGAGCAGCACGGCCGACGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

P_AAX28433 1 GGCCGGAGCAGCACGGCCGACGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

P_AAX28433 61 CGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292 121 GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

P_AAX28433 121 GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAAGTTTGGCGGCGGGAACACGGC

P_AAX28433 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAAGTTTGGCGGCGGGAACACGGC

DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

P_AAX28433 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

P_AAX28433 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

BLAST RESULTS A-11

P_AAX28433	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC *****
P_AAX28433	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG *****
P_AAX28433	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA *****
P_AAX28433	541	CAGACAGGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG *****
P_AAX28433	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT *****
P_AAX28433	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC *****
P_AAX28433	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG *****
P_AAX28433	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC *****
P_AAX28433	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA *****
P_AAX28433	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG *****
P_AAX28433	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC *****
P_AAX28433	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC *****
P_AAX28433	1081	AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292	1141	CCTTTAAATTATTTCAGAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT *****
P_AAX28433	1141	CCTTTAAATTATTTCAGAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC *****
P_AAX28433	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

BLAST RESULTS A-12

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DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
P_AAX28433 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
*****
P_AAX28433 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>8 P_AAX52213 Protein PRO211 cDNA clone DNA32292-1131. DNA, PAT 25-JUN-1999
(1364 bp) [1 seg]
Score = 1364 (2704 bits), Expect = 0.0
Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/+

DNA32292 1 GCCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAX52213 1 GCCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAX52213 61 CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

DNA32292 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
*****
P_AAX52213 121 GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
*****
P_AAX52213 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
*****
P_AAX52213 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAX52213 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAX52213 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

DNA32292 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****
P_AAX52213 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC

DNA32292 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
*****
P_AAX52213 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG

DNA32292 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCGCTGTGCACTGA
*****
P_AAX52213 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCGCTGTGCACTGA

DNA32292 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
*****
P_AAX52213 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

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BLAST RESULTS A-13

DNA32292 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

 P_AAX52213 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
 DNA32292 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

 P_AAX52213 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
 DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

 P_AAX52213 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
 DNA32292 841 TGA CTCCAGCTGTGTGGGTGTCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC

 P_AAX52213 841 TGA CTCCAGCTGTGTGGGTGTCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
 DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA

 P_AAX52213 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
 DNA32292 961 AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

 P_AAX52213 961 AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
 DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

 P_AAX52213 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
 DNA32292 1081 AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

 P_AAX52213 1081 AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
 DNA32292 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGAAAAATGTGGCCCTGAGGATGCCGTCTCCT

 P_AAX52213 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGAAAAATGTGGCCCTGAGGATGCCGTCTCCT
 DNA32292 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

 P_AAX52213 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
 DNA32292 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

 P_AAX52213 1261 TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
 DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

 P_AAX52213 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>9 P_AAX37671 Human EGF-like homologue (PRO217) encoded by DNA32292 cDNA. (1364 bp) [1 seg]
 Score = 1364 (2704 bits), Expect = 0.0
 Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/+

DNA32292 1 GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

 P_AAX37671 1 GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

BLAST RESULTS A-14

DNA32292	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

P_AAX37671	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

P_AAX37671	121	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

P_AAX37671	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT

P_AAX37671	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCAATGCAATCAGATGCTAGAGGCGCAGGAGGA

P_AAX37671	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT

P_AAX37671	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC

P_AAX37671	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG

P_AAX37671	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA

P_AAX37671	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

P_AAX37671	601	CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

P_AAX37671	661	TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

P_AAX37671	721	GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

P_AAX37671	781	TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC

P_AAX37671	841	TGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC

BLAST RESULTS A-15

DNA32292	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA

P_AAX37671	901	TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAA
DNA32292	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

P_AAX37671	961	AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

P_AAX37671	1021	TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292	1081	AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

P_AAX37671	1081	AGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292	1141	CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT

P_AAX37671	1141	CCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC

P_AAX37671	1201	GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
DNA32292	1261	TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

P_AAX37671	1261	TTAAACAGCTGCATTTCTTGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
DNA32292	1321	TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

P_AAX37671	1321	TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>10 AX076909 Sequence 21 from Patent WO0105836. (1364 bp) [1 seg]
 Score = 1364 (2704 bits), Expect = 0.0
 Identities = 1364/1364 (100%), at 1,1-1364,1364, Strand +/+

DNA32292	1	GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC

AX076909	1	GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC

AX076909	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA

AX076909	121	GCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC

AX076909	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT

AX076909	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA

BLAST RESULTS A-10


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*****
AX076909 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
AX076909 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****
AX076909 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
*****
AX076909 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCGCTGTGCACTGA
*****
AX076909 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCGCTGTGCACTGA
DNA32292 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
*****
AX076909 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
*****
AX076909 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
*****
AX076909 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
*****
AX076909 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
*****
AX076909 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
*****
AX076909 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292 961 AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
*****
AX076909 961 AACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
*****
AX076909 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292 1081 AGAAGGAGAAAAGCCCCGACACAGCTGCCCTCCCGCAAGACCTGTAATGTGCCGGACTTAC
*****
AX076909 1081 AGAAGGAGAAAAGCCCCGACACAGCTGCCCTCCCGCAAGACCTGTAATGTGCCGGACTTAC
DNA32292 1141 CCTTTAAATTATTCAGAAGGATGTCCCGTGGAAAAATGTGGCCCTGAGGATGCCGTCTCCT
*****

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BLAST RESULTS A-17

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AX076909 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
*****
AX076909 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC
DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
*****
AX076909 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
DNA32292 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAA
*****
AX076909 1321 TGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAA

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>11 P_AAF29457 Human TANGO 331 cDNA. (1432 bp) [1 seg]
Score = 1350 (2676 bits), Expect = 0.0
Identities = 1350/1350 (100%), at 1,50-1350,1399, Strand +/-

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DNA32292 1 GGCCGGAGCAGCACGGCCGCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
*****
P_AAF29457 50 GGCCGGAGCAGCACGGCCGCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292 61 CGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
*****
P_AAF29457 110 CGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292 121 GCCCGCGCCGGAGGCCGCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGG
*****
P_AAF29457 170 GCCCGCGCCGGAGGCCGCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGG
DNA32292 181 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGGAACACGGC
*****
P_AAF29457 230 CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGGAACACGGC
DNA32292 241 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
*****
P_AAF29457 290 TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
DNA32292 301 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
*****
P_AAF29457 350 GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292 361 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
*****
P_AAF29457 410 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292 421 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
*****
P_AAF29457 470 TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292 481 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
*****
P_AAF29457 530 ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292 541 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCGCTGTGCACTGA
*****
P_AAF29457 590 CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCGCTGTGCACTGA

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BLAST RESULTS A-10

DNA32292 601 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG

P_AAF29457 650 CTGCATGGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTG
DNA32292 661 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT

P_AAF29457 710 TGACGAGTCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGT
DNA32292 721 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC

P_AAF29457 770 GGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCC
DNA32292 781 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG

P_AAF29457 830 TCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTG
DNA32292 841 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC

P_AAF29457 890 TGA CTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTC
DNA32292 901 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA

P_AAF29457 950 TGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAA
DNA32292 961 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG

P_AAF29457 1010 AACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTG
DNA32292 1021 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC

P_AAF29457 1070 TCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCAC
DNA32292 1081 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC

P_AAF29457 1130 AGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTAC
DNA32292 1141 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT

P_AAF29457 1190 CCTTTAAATTATTTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCTCCT
DNA32292 1201 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC

P_AAF29457 1250 GCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC
DNA32292 1261 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT

P_AAF29457 1310 TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTT
DNA32292 1321 TGTAAATAAAATTGACCATTGTAGGTAATCA

P_AAF29457 1370 TGTAAATAAAATTGACCATTGTAGGTAATCA

Blast Results A-19

>12 P_AAA08503 DNA encoding human apoptosis related protein. (1380 bp) [1 seg]
Score = 1290 (2557 bits), Expect = 0.0
Identities = 1358/1369 (99%), Gaps = 10/1369 (0%), at 1,10-1364,1373, Strand
+/+

DNA32292	1	GGCCGGAGCAGCACGGCCGCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
P_AAA08503	10	GGCCGGAGCAGCACGGCCGCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACC
DNA32292	61	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
P_AAA08503	70	CGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCC
DNA32292	121	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
P_AAA08503	130	GCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGA
DNA32292	181	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
P_AAA08503	190	CAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGC
DNA32292	241	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
P_AAA08503	250	TTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCT
DNA32292	301	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
P_AAA08503	310	GGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
DNA32292	361	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
P_AAA08503	370	GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTT
DNA32292	421	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
P_AAA08503	430	TTGTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGC
DNA32292	481	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
P_AAA08503	490	ATGCCAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAG
DNA32292	541	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
P_AAA08503	550	CAGACAGGGCGACGGGTCCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGA
DNA32292	601	CTGCATGGACGGCTACTTCAGCT-CGCTCCGG-AACGAGACCCACAGCATCTGCACAGCC
P_AAA08503	610	CTGCATGGACGGCTACTTCAGCTCCGCTCCGGRAACGAGACCCACAGCATCTGCACAGCC
DNA32292	659	TGTGACGAGTCCTGCAAGACGTGCTC-GGGCCT-GACCAACAGAGAC-TGCGGCGAGTGT
P_AAA08503	670	TGTGACGAGTCCTGCAAGACGTGCTCGGGGCCCTGGACCAACAGAGACTTGCGGCGAGTGT
DNA32292	716	GAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAG
P_AAA08503	730	GAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGA-
DNA32292	776	CCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAA
P_AAA08503	789	CCG--TCCCTGCAGCG-TGC-CAGTTCTGTAAGAACCCCAACGGCTCCTACACGTGCGAA

BLAST RESULTS A-20

DNA32292	836	GAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGT
P_AAA08503	845	GAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGT
DNA32292	896	ATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCA
P_AAA08503	905	ATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCA
DNA32292	956	GAAAAAACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGT
P_AAA08503	965	GAAAAAACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTACGTCTGT
DNA32292	1016	GTGTGTCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAA
P_AAA08503	1025	GTGTGTCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAA
DNA32292	1076	GCCACAGAAGGAGAAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGA
P_AAA08503	1085	GCCACAGAAGGAGAAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGGA
DNA32292	1136	CTTACCCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGT
P_AAA08503	1145	CTTACCCTTTAAATTATTTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGT
DNA32292	1196	CTCCTGCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTT
P_AAA08503	1205	CTCCTGCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTT
DNA32292	1256	GTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAG
P_AAA08503	1265	GTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAG
DNA32292	1316	TTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA
P_AAA08503	1325	TTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

>13 P_AAC76920 Human ORFX ORF2475 polynucleotide sequence SEQ ID NO:4949. (1259 bp) [1 seg]

Score = 1208 (2395 bits), Expect = 0.0

Identities = 1215/1216 (99%), Gaps = 1/1216 (0%), at 150,32-1364,1247, Strand +/+

DNA32292	150	CGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAACCAGGGGATGGTGGACACCG
P_AAC76920	32	CGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAACCAGGGGATGGTGGACACCG
DNA32292	210	CAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAAGACGCTGTCCAAGTACG
P_AAC76920	92	CAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAAGACGCTGTCCAAGTACG
DNA32292	270	AGTCCAGCGAGATTTCGCTGCTGGAGATCCTGGAGGGGCTGTGCGAGAGCAGCGACTTCG
P_AAC76920	152	AGTCCAGCGAGATTTCGCTGCTGGAGATCCTGGAGGGGCTGTGCGAGAGCAGCGACTTCG
DNA32292	330	AATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTGGCTGCAGCTGA
P_AAC76920	212	AATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTGGCTGCAGCTGA

BLAST RESULTS A-21

DNA32292	390	AGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGTGTGCTGCT
P_AAC76920	272	AGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGTGTGCTGCT
DNA32292	450	CTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCCCTGCA
P_AAC76920	332	CTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCCCTGCA
DNA32292	510	GCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTGCCGGTGCC
P_AAC76920	392	GCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTGCCGGTGCC
DNA32292	570	ACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCC
P_AAC76920	452	ACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCC
DNA32292	630	GGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCC
P_AAC76920	512	GGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCC
DNA32292	690	TGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTG
P_AAC76920	572	TGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTG
DNA32292	750	TGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGA
P_AAC76920	632	TGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGA
DNA32292	810	ACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGG
P_AAC76920	692	ACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGG
DNA32292	870	AAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTG
P_AAC76920	752	AAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTG
DNA32292	930	CAGATGTGGACGAGTGTCTACTAGCAGAAAAACCTGTGTGAGGAAAAACGAAACTGCT
P_AAC76920	812	CAGATGTGGACGAGTGTCTACTAGCAGAAAAACCTGTGTGAGGAAAAACGAAACTGCT
DNA32292	990	ACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTTGACGGCTTCGAAGAA-ACGGAAGAT
P_AAC76920	872	ACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTTGACGGCTTCGAAGAANACGGAAGAT
DNA32292	1049	GCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCC
P_AAC76920	932	GCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCC
DNA32292	1109	TCCCGCGAAGACCTGTAATGTGCCGGAATTACCCTTTAAATTATTCAGAAGGATGTCCCG
P_AAC76920	992	TCCCGCGAAGACCTGTAATGTGCCGGAATTACCCTTTAAATTATTCAGAAGGATGTCCCG
DNA32292	1169	TGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC
P_AAC76920	1052	TGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC

BLAST RESULTS A-22

DNA32292	1229	CTGCTCTCTAACGGTTGATTCTCATTGTGCCCTTAAACAGCTGCATTTCTTGGTTGTTCT

P_AAC76920	1112	CTGCTCTCTAACGGTTGATTCTCATTGTGCCCTTAAACAGCTGCATTTCTTGGTTGTTCT
DNA32292	1289	TAAACAGACTTGTATATTTTGATACAGTTCCTTGTAAATAAAATTGACCATTGTAGGTAAT

P_AAC76920	1172	TAAACAGACTTGTATATTTTGATACAGTTCCTTGTAAATAAAATTGACCATTGTAGGTAAT
DNA32292	1349	CAGGAGGAAAAAAAAA

P_AAC76920	1232	CAGGAGGAAAAAAAAA

BLAST RESULTS A-23

(B)

Tue Jul 17 13:23:35 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpanda/templ/pl.DNA32292.nc (353 aa)

Sequences producing High-scoring Segment Pairs:	Score	Match	Pct	E-val
1 P_AAB53075 Human angiogenesis-associated protein PRO	2005	353	100	0.0
2 P_AAB61231 Human TANGO 331 protein - Homo sapiens.	2005	353	100	0.0
3 P_AAB80212 Human PRO211 protein - Homo sapiens.	2005	353	100	0.0
4 P_AAB68596 PRO211 - Homo sapiens.	2005	353	100	0.0
5 P_AAY83224 PRO211 Polypeptide - Homo sapiens.	2005	353	100	0.0
6 P_AAB00169 PRO211 polypeptide - Homo sapiens.	2005	353	100	0.0
7 P_AAY05283 EGF-like homologue PRO211 - Homo sapiens.	2005	353	100	0.0
8 P_AAY13344 protein PRO211 - Homo sapiens.	2005	353	100	0.0
9 P_AAY08064 Human EGF-like homologue protein (PRO217)	2005	353	100	0.0
10 P_AAY88571 Human PRO211 amino acid sequence - Homo s	1997	352	100	0.0
11 P_AAB61233 Mature human TANGO 331 protein - Homo sap	1887	329	100	0.0
12 AAH02894.114 Unknown (protein for MGC:11256) - Homo sa	1770	321	91	0.0
13 NP_077300.1 hypothetical protein MGC11256 - Homo sapi	1770	321	91	0.0
14 P_AAB42711 Human ORFX ORF2475 polypeptide sequence S	1716	298	97	0.0
15 P_AAY91870 Human apoptosis related protein - Homo sa	1635	301	85	0.0

BLAST RESULTS B-1

>1 P_AAB53075 Human angiogenesis-associated protein PRO211, SEQ ID NO:57 - Homo sapiens. (353 aa) [1 seg]

Score = 2005 (776 bits), Expect = 0.0

Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

DNA32292.nc	1	MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

P_AAB53075	1	MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc	61	EEKTLISKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

P_AAB53075	61	EEKTLISKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc	121	VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC

P_AAB53075	121	VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC
DNA32292.nc	181	MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP

P_AAB53075	181	MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc	241	CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT

P_AAB53075	241	CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
DNA32292.nc	301	CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL

P_AAB53075	301	CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL

>2 P_AAB61231 Human TANGO 331 protein - Homo sapiens. (353 aa) [1 seg]

Score = 2005 (776 bits), Expect = 0.0

Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

DNA32292.nc	1	MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

P_AAB61231 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

P_AAB61231 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC

P_AAB61231 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP

P_AAB61231 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA

P_AAB61231 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

P_AAB61231 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

>3 P_AAB80212 Human PRO211 protein - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

P_AAB80212 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

P_AAB80212 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC

P_AAB80212 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP

P_AAB80212 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA

P_AAB80212 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

P_AAB80212 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

>4 P_AAB68596 PRO211 - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

P_AAB68596 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW

BLAST RESULTS B-2

```

DNA32292.nc 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAB68596 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAB68596 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPP
*****
P_AAB68596 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPP
*****
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAECT
*****
P_AAB68596 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAECT
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAB68596 301 CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL
*****

```

>5 P_AAY83224 PRO211 Polypeptide - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY83224 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
DNA32292.nc 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAY83224 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY83224 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPP
*****
P_AAY83224 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPP
*****
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAECT
*****
P_AAY83224 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAECT
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY83224 301 CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL
*****

```

>6 P_AAB00169 PRO211 polypeptide - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAB00169 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****

```

BLAST RESULTS B-3

```

DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAB00169 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC
*****
P_AAB00169 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC
*****
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAB00169 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAB00169 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAB00169 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****

```

>7 P_AAY05283 EGF-like homologue PRO211 - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY05283 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAY05283 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC
*****
P_AAY05283 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDC
*****
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAY05283 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAY05283 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY05283 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****

```

>8 P_AAY13344 protein PRO211 - Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY13344 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****

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BLAST RESULTS B-A

```

*****
P_AAY13344 61 EEKTLKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGGSRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY13344 121 VKTLKVCCSPGTYGPDCLACQGGGSRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAY13344 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAY13344 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY13344 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

```

>9 P_AAY08064 Human EGF-like homologue protein (PRO217) encoded by DNA32292 cDNA
- Homo sapiens. (353 aa) [1 seg]
Score = 2005 (776 bits), Expect = 0.0
Identities = 353/353 (100%), Positives = 353/353 (100%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY08064 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc 61 EEKTLKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAY08064 61 EEKTLKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGGSRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY08064 121 VKTLKVCCSPGTYGPDCLACQGGGSRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAY08064 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAY08064 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY08064 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

```

>10 P_AAY88571 Human PRO211 amino acid sequence - Homo sapiens. (353 aa) [1 seg]
Score = 1997 (773 bits), Expect = 0.0
Identities = 352/353 (99%), Positives = 352/353 (99%), at 1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY88571 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc 61 EEKTLKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

```

BLAST RESULTS B-5

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*****
P_AAY88571 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY88571 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAY88571 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
P_AAY88571 241 CSAAQFCKMANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY88571 301 CVRKNENCYNTPGSYVCVCPDGFETEDACVPPAEAEATEGESPTQLPSREDL

```

>11 P_AAB61233 Mature human TANGO 331 protein - Homo sapiens. (329 aa) [1 seg]
Score = 1887 (731 bits), Expect = 0.0
Identities = 329/329 (100%), Positives = 329/329 (100%), at 25,1-353,329

```

DNA32292.nc 25 AKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEKTL SKYESSEIRLLEILEGLCE
*****
P_AAB61233 1 AKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEKTL SKYESSEIRLLEILEGLCE
DNA32292.nc 85 SSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGG
*****
P_AAB61233 61 SSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGG
DNA32292.nc 145 QRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDCMDGYFSSLRNETHSICTACDESK
*****
P_AAB61233 121 QRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDCMDGYFSSLRNETHSICTACDESK
DNA32292.nc 205 TCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAB61233 181 TCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
DNA32292.nc 265 GCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
*****
P_AAB61233 241 GCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
*****
DNA32292.nc 325 ETEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAB61233 301 ETEDACVPPAEAEATEGESPTQLPSREDL

```

>12 AAH02894.114 Unknown (protein for MGC:11256) - Homo sapiens (321 aa) [1 seg]
Score = 1770 (686 bits), Expect = 0.0
Identities = 321/353 (90%), Positives = 321/353 (90%), Gaps = 32/353 (9%), at 1,1-353,321

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
AAH02894.114 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc 61 EEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC

```

BLAST RESULTS B-U

```

*****
AAH02894.114 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
AAH02894.114 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
AAH02894.114 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
AAH02894.114 241 CSAAQFCKNANGSYTCE-----DVDECSLA
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
AAH02894.114 269 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

```

>13 NP_077300.1 hypothetical protein MGC11256 - Homo sapiens (321 aa) [1 seg]
Score = 1770 (686 bits), Expect = 0.0
Identities = 321/353 (90%), Positives = 321/353 (90%), Gaps = 32/353 (9%), at 1,1-353,321

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
NP_077300.1 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
DNA32292.nc 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
NP_077300.1 61 EEKTLKSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
NP_077300.1 121 VKTLKVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
DNA32292.nc 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
NP_077300.1 181 MDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
DNA32292.nc 241 CSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA
*****
NP_077300.1 241 CSAAQFCKNANGSYTCE-----DVDECSLA
*****
DNA32292.nc 301 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL
*****
NP_077300.1 269 CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

```

>14 P_AAB42711 Human ORFX ORF2475 polypeptide sequence SEQ ID NO:4950 - Homo (318 aa) [1 seg]
Score = 1716 (665 bits), Expect = 0.0
Identities = 298/306 (97%), Positives = 298/306 (97%), at 20,2-325,307

```

DNA32292.nc 20 PAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLKSKYESSEIRLLEIL
**
P_AAB42711 2 PACPPGYLTAPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLKSKYESSEIRLLEIL

```

BLAST RESULTS B-7

```

DNA32292.nc 80 EGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLA
*****
P_AAB42711 62 EGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLA
*****
DNA32292.nc 140 CQGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDCMDGYFSSLRNETHSICTAC
*****
P_AAB42711 122 CQGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDCMDGYFSSLRNETHSICTAC
*****
DNA32292.nc 200 DESCKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANGSYTCEEC
*****
P_AAB42711 182 DESCKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANGSYTCEEC
*****
DNA32292.nc 260 DSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT CVRKNENCYNTPGSYVCVC
*****
P_AAB42711 242 DSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT CVRKNENCYNTPGSYVCVC
*****
DNA32292.nc 320 PDGFEE
*****
P_AAB42711 302 PDGFEE

```

>15 P_AAY91870 Human apoptosis related protein - Homo sapiens. (353 aa) [1 seg]
Score = 1635 (634 bits), Expect = 0.0
Identities = 301/354 (85%), Positives = 306/354 (86%), Gaps = 2/354 (0%), at
1,1-353,353

```

DNA32292.nc 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
P_AAY91870 1 MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW
*****
DNA32292.nc 61 EEKTLKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
P_AAY91870 61 EEKTLKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFC
*****
DNA32292.nc 121 VKTLKVCCSPGTYGPDCLACQGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
P_AAY91870 121 VKTLKVCCSPGTYGPDCLACQGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGGLCTDC
*****
DNA32292.nc 181 MDGYFSSL-RNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEP
*****
P_AAY91870 181 MDGYFSSAPXTRPTASAQPVTSPARRARGLDQORLA-ASVKWAGCWTRAPVWMWTSVRPT
*****
DNA32292.nc 240 PCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEK
*****
P_AAY91870 240 VPAACQFCKNPNGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEK
*****
DNA32292.nc 300 TCVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL
*****
P_AAY91870 300 TCVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL

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